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LOCUS AE000479 10934 bp DNA linear BCT 01-DEC-2000

DEFINITION Escherichia coli K12 MG1655 section 369 of 400 of the complete genome.

ACCESSION AE000479 U00096

VERSION AE000479.1

KEYWORDS .

SOURCE Escherichia coli K12

ORGANISM Escherichia coli K12

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

REFERENCE 1 (bases 1 to 10934)

AUTHORS Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.

TITLE The complete genome sequence of Escherichia coli K-12

JOURNAL Science 277 (5331), 1453-1474 (1997)

MEDLINE 97426617

PUBMED 9278503

REFERENCE 2 (bases 1 to 10934)

AUTHORS Blattner, F.R.

TITLE Direct Submission

JOURNAL Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459

REFERENCE 3 (bases 1 to 10934)

AUTHORS Blattner, F.R.

TITLE Direct Submission

JOURNAL Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459

REFERENCE 4 (bases 1 to 10934)

AUTHORS Plunkett, G. III.

TITLE Direct Submission

JOURNAL Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

COMMENT On Sep 9, 1997 this sequence version replaced gi:1790489. This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@amher.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (<http://cgsc.biology.yale.edu>). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site (<http://www.genetics.wisc.edu>). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated

sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein- or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene names.

| FEATURES | Location/Qualifiers |
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| <u>source</u> | 1..10934 /organism="Escherichia coli K12" /strain="K12" /sub_strain="MG1655" /db_xref="taxon:83333" |
| <u>protein_bind</u> | 118..140 /note="central position to predicted promoter: -202.5" /bound_moiety="GlpR predicted site" |
| <u>promoter</u> | 298..326 /note="factor Sigma70; predicted +1 start at 4266933" |
| <u>protein_bind</u> | 310..337 /note="central position to predicted promoter: -8" /bound_moiety="DeoR predicted site" |
| <u>gene</u> | 393..1106 /gene="aphA" /note="synonym: b4055" |
| <u>CDS</u> | 393..1106 /gene="aphA" /function="enzyme; Central intermediary metabolism: Nucleotide hydrolysis" /note="o237; sequence change joins two ORFs relative to earlier version; 99.2 pct identical to the conceptual ORF YJBP_ECOLI SW:P32697" /codon_start=1 /transl_table=11 /product="diadenosine tetraphosphatase" /protein_id="AAC77025.1" /db_xref="GI:2367341" /translation="MRKITQAISAVCLLFALNSSAVALASSPSPLNPGTNVARLAEQA PIHWVSVAQIENSLAGRPPMAVGFDIDDTVLFSSPGFWRGKKTFSPESEDYLNPNVFW EKMNNGWDEFSIPKEVARQLIDMHVRRGDAIFFVTGRSPTKTETVSKTLADNFHIPAT NMNPVIFAGDKPGQNTKSQWLQDKNIRIFYGSDNDITAARDVGARGIRILRASNSTY KLPQAGAFGEVIVNSEY" |
| <u>promoter</u> | 1174..1202 /note="factor Sigma70; predicted +1 start at 4267809" |
| <u>gene</u> | 1217..1633 /gene="yjbQ" /note="synonym: b4056" |
| <u>CDS</u> | 1217..1633 /gene="yjbQ" /function="orf; Unknown" /note="o138; 100 pct identical amino acid sequence and equal length to YJBQ_ECOLI SW: P32698" /codon_start=1 /transl_table=11 /product="orf, hypothetical protein" /protein_id="AAC77026.1" /db_xref="GI:1790491" /translation="MWYQKTLTSAKSRGFHLVTDEILNQLADMPRVNIGLLHLLQLH TSASLTLENCDPTVRHDMERFFLRTPDNGNYEHYEGADDMPSHIKSSMLGTSLVL PVHKGRIQTGTWQGIWLGEHR IHGGSRRRIATLQGE" |
| <u>gene</u> | 1637..1993 /gene="yjbR" /note="synonym: b4057" |
| <u>CDS</u> | 1637..1993 /gene="yjbR" /function="orf; Unknown" /note="o118; 100 pct identical amino acid sequence and equal length to YJBR_ECOLI SW: P32699" /codon_start=1 /transl_table=11 /product="orf, hypothetical protein" /protein_id="AAC77027.1" /db_xref="GI:2367342" /translation="MTISELLQYCMAPGAEQSVHNDWKATQIKVEDVLFAMVKEVEN" |

RPAVSLKTSPELAELLRQQHSDVRPSRHLNKAHWSTVYLDGSLPDSQIYYLVDSYQQ
 AVNLLPEEKRLLVQL"
gene complement(2028..4850)
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 /note="synonym: b4058"
CDS complement(2028..4850)
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 /function="enzyme; DNA - replication, repair,
 restriction/modification"
 /note="o940; 99 pct identical amino acid sequence and
 equal length to UVRA_ECOLI SW: P07671; CG Site No. 21"
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 EIH DYLRLLFARVGEPRCPDHDVPLAAQTVSQMVDNVLSQPEGKRLMLLAPI IKERKG
 EHTKTLENLASQGYIRARIDGEVCDLSDPPKLELQKKHTIEVVDRFKVRDDLTQRLA
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promoter complement(4901..4927)
 /note="factor Sigma70; promoter uvrA; documented +1 at
 4271488"
protein_bind complement(4909..4929)
 /note="central position to uvrA promoter: -10.5"
 /bound_moiety="LexA documented site"
protein_bind 4934..4954
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promoter 4948..4978
 /note="factor Sigma70; promoter ssb; documented +1
 at4271590"
promoter 5026..5055
 /note="factor Sigma70; promoter ssbp2; documented +1
 at4271663"
promoter 5041..5069
 /note="factor Sigma70; promoter ssbp3; documented +1
 at4271674"
gene 5104..5640
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CDS 5104..5640
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 restriction/modification"
 /note="o178; CG Site No. 150"
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 PAAPSNEPPMDFDDDI PF"
gene complement(5739..6089)
 /gene="yjcB"
 /note="synonym: b4060"

CDS complement(5739..6089)
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 /function="orf; Unknown"
 /note="f116; 100 pct identical amino acid sequence and equal length to YJCB_ECOLI SW: P32700"
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 /db_xref="GI:1790495"
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 EMNQTPPQWPMILT"

protein_bind 6146..6174
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 /bound_moiety="GalR predicted site"

protein_bind 6146..6174
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 /bound_moiety="GalR predicted site"

promoter complement(6156..6185)
 /note="factor Sigma70; predicted +1 start at 4272749"

promoter 6280..6307
 /note="factor Sigma70; predicted +1 start at 4272914"

protein_bind 6323..6345
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 /bound_moiety="Fur predicted site"

protein_bind 6323..6345
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promoter 6339..6370
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gene 6450..8036
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 /note="synonym: b4061"

CDS 6450..8036
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 FWSEVMSDDPTLQWGVYDVTYKTFSSLKEASAATFSPILHLKDLTVQRNGLYATVY
 STKRPIAAIVATSYQRLITHFYNHLIFALPAGILGSLVLLLWLRIQNYLSPKRKLQ
 RALEKHQLCLLYQPIIDIKTEKIGAEALLRWPGEQQIMNPAEFLPLAEKEGMIEQI
 TDYVIDNVFRDLGDYLATHADRYVSNLSASDFHTSRLIARINQKTEQYAVRPQKIKF
 EVTEHAFLDVKMTPILAFRQAGYEVAIDDFGIGYSNLHNLKSLNVDILKIDKSFE
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gene complement(8039..8362)
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CDS complement(8039..8362)
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 /db_xref="GI:1790497"
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 YRHRL"

promoter 8388..8416
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promoter complement(8409..8438)
 /note="factor Sigma70; predicted +1 start at 4275002"
protein_bind complement(8442..8471)
 /note="central position to soxS promoter: -26"
 /bound_moiety="SoxS documented site"
gene 8448..8912
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CDS 8448..8912
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 /function="regulator; Global regulatory functions"
 /note="o154; 100 pct identical amino acid sequence and equal length to SOXR_ECOLI SW: P22538"
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 /transl_table=11
 /product="redox-sensing activator of soxS"
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 /db_xref="GI:1790498"
 /translation="MEKKLPRIKALLTPGEVAKRSGVAVSALHFYESKGLITSIRNSG
 NQRRYKRDVLRVYVAIKIAQRIGIPLATIGEAFGVLPEGHTLSAKEWKQLSSQWREEL
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promoter 9261..9290
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gene 9458..10807
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